Supplementary Table S3 Statistical table of sequence alignment between sample sequencing data and reference genomes.

Sample	Total Reads	Mapped Reads	Uniq Mapped Reads	Multiple Map Reads	Reads Map to '+'	Reads Map to '-'
CT5-10-1	49,367,574	46,003,473 (93.19%)	44,588,060 (90.32%)	1,415,413 (2.87%)	23,808,449 (48.23%)	23,842,714 (48.30%)
CT5-10-2	46,367,444	43,367,355 (93.53%)	42,013,133 (90.61%)	1,354,222 (2.92%)	22,463,087 (48.45%)	22,487,878 (48.50%)
CT5-10-3	48,905,216	46,336,544 (94.75%)	44,863,684 (91.74%)	1,472,860 (3.01%)	23,994,127 (49.06%)	24,035,871 (49.15%)
CT5-5-1	43,331,146	40,048,239 (92.42%)	38,651,991 (89.20%)	1,396,248 (3.22%)	20,797,924 (48.00%)	20,836,478 (48.09%)
CT5-5-2	40,695,450	38,739,802 (95.19%)	37,330,471 (91.73%)	1,409,331 (3.46%)	20,160,901 (49.54%)	20,174,959 (49.58%)
CT5-5-3	42,320,140	38,169,819 (90.19%)	36,955,786 (87.32%)	1,214,033 (2.87%)	19,778,348 (46.74%)	19,806,590 (46.80%

Note: (1) Sample: sample analysis number;

(2) Total Reads: Number of Clean Reads in a single end;

(3) Mapped Reads: number of Reads mapped to the reference genome and percentage of Clean Reads;

(4) Uniq Mapped Reads: Number of Reads aligned to unique locations in the reference genome and percentage of Clean Reads;

(5) Multiple Map Reads: The number of Reads that were compared to multiple locations of the reference genome and the percentage of Clean Reads;

(6) Reads Map to '+' : The number of Reads linked to the positive strand of the reference genome and the percentage of Clean Reads;

(7) Reads Map to '-' : The number of Reads with negative chains in the reference genome and the percentage of Clean Reads.